



#14

SEQUENCE LISTING

<110> Prayaga, Suhhirdas K
Shimkets, Richard A

<120> Novel Polypeptides and Polynucleotides Encoding Same

<130> 15966-615

<140> 09/732,436

<141> 2000-12-07

<150> 60/169,887

<151> 1999-12-09

<150> 60/170,230

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<170> PatentIn Ver. 2.1

<210> 1

<211> 475

<212> DNA

<213> Homo sapiens

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<210> 2

<211> 154

<212> PRT

<213> Homo sapiens

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1 5 10 15
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20 25 30
 Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser
 35 40 45
 Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His
 50 55 60
 Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys
 65 70 75 80
 Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg
 85 90 95
 Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn
 100 105 110
 Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr
 115 120 125
 Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn
 130 135 140
 Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu
 145 150

<210> 3
 <211> 610
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (74)..(208)
 <223> Wherein n is a or t or c or g.

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 gcaccagcag atcttcagcc tctttttaca caagggttg tctgatgctt ggaatagggc 300
 cttctctggac aaactccaga ctggatttca tcagcagctg gaagacctgg agacctgctt 360
 tggatatagag gatgggaagc aagagtctgc cctggaaatt gagggcccta cactggccat 420
 aaagaggtac ttccagggag tacatttctt cttgaaagag aggaaattca ggaactgtac 480
 ctgggaggtt gtcgtaatgg taaagggtt tttcttaagc acaaaaacttc aagaaaaaga 540
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gtgaaagctg

610

<210> 4

<211> 199

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (24)..(68)

<223> Wherein Xaa is any amino acid.

<400> 4

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20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His
65 70 75 80

Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp
85 90 95

Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu
100 105 110

Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser
115 120 125

Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln
130 135 140

Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp
145 150 155 160

Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln
165 170 175

Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys

180

185

190

Val Ile Tyr Leu Ala Glu Glu

195

<210> 5

<211> 1887

<212> DNA

<213> Homo sapiens

<400> 5

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1887

<210> 6

<211> 628

<212> PRT

<213> Homo sapiens

<400> 6

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			20					25					30			
Arg	Cys	Gln	Thr	Gln	Ser	Leu	Pro	Leu	Ser	Val	Leu	Cys	Pro	Gly	Ala	
		35					40					45				
Gly	Leu	Leu	Phe	Val	Pro	Pro	Ser	Leu	Asp	Arg	Arg	Ala	Ala	Glu	Leu	
	50					55					60					
Arg	Leu	Ala	Asp	Asn	Phe	Ile	Ala	Ser	Val	Arg	Arg	Arg	Asp	Leu	Ala	
65					70					75					80	
Asn	Met	Thr	Gly	Leu	Leu	His	Leu	Ser	Leu	Ser	Arg	Asn	Thr	Ile	Arg	
				85					90					95		
His	Val	Ala	Ala	Gly	Ala	Phe	Ala	Asp	Leu	Arg	Ala	Leu	Arg	Ala	Leu	
		100						105					110			
His	Leu	Asp	Gly	Asn	Arg	Leu	Thr	Ser	Leu	Gly	Glu	Gly	Gln	Leu	Arg	
	115						120					125				
Gly	Leu	Val	Asn	Leu	Arg	His	Leu	Ile	Leu	Ser	Asn	Asn	Gln	Leu	Ala	
	130					135					140					
Ala	Leu	Ala	Ala	Gly	Ala	Leu	Asp	Asp	Cys	Ala	Glu	Thr	Leu	Glu	Asp	
145					150					155					160	
Leu	Asp	Leu	Ser	Tyr	Asn	Asn	Leu	Glu	Gln	Leu	Pro	Trp	Glu	Ala	Leu	
				165					170					175		
Gly	Arg	Leu	Gly	Asn	Val	Asn	Thr	Leu	Gly	Leu	Asp	His	Asn	Leu	Leu	
		180						185					190			
Ala	Ser	Val	Pro	Ala	Gly	Ala	Phe	Ser	Arg	Leu	His	Lys	Leu	Ala	Arg	
		195					200					205				
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Phe	Ser	Arg	Leu	Pro	Leu	Leu	Ala	Arg	Pro	Arg	Gly	Ser	Pro	Ala	Ser	
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Ala	Leu	Val	Leu	Ala	Phe	Gly	Gly	Asn	Pro	Leu	His	Cys	Asn	Cys	Glu	245	250	255
Leu	Val	Trp	Leu	Arg	Arg	Leu	Ala	Arg	Glu	Asp	Asp	Leu	Glu	Ala	Cys	260	265	270
Ala	Ser	Pro	Pro	Ala	Leu	Gly	Gly	Arg	Tyr	Phe	Trp	Ala	Val	Gly	Glu	275	280	285
Glu	Glu	Phe	Val	Cys	Glu	Pro	Pro	Val	Val	Thr	His	Arg	Ser	Pro	Pro	290	295	300
Leu	Ala	Val	Pro	Ala	Gly	Arg	Pro	Ala	Ala	Leu	Arg	Cys	Arg	Ala	Val	305	310	315
Gly	Asp	Pro	Glu	Pro	Arg	Val	Arg	Trp	Val	Ser	Pro	Gln	Gly	Arg	Leu	325	330	335
Leu	Gly	Asn	Ser	Ser	Arg	Ala	Arg	Ala	Phe	Pro	Asn	Gly	Thr	Leu	Glu	340	345	350
Leu	Leu	Val	Thr	Glu	Pro	Gly	Asp	Gly	Gly	Ile	Phe	Thr	Cys	Ile	Ala	355	360	365
Ala	Asn	Ala	Ala	Gly	Glu	Ala	Thr	Ala	Ala	Val	Glu	Leu	Thr	Val	Gly	370	375	380
Pro	Pro	Pro	Pro	Pro	Gln	Leu	Ala	Asn	Ser	Thr	Ser	Cys	Asp	Pro	Pro	385	390	395
Arg	Asp	Gly	Asp	Pro	Asp	Ala	Leu	Thr	Pro	Pro	Ser	Ala	Ala	Ser	Ala	405	410	415
Ser	Ala	Lys	Val	Ala	Asp	Thr	Gly	Pro	Pro	Thr	Asp	Arg	Gly	Val	Gln	420	425	430
Val	Thr	Glu	His	Gly	Ala	Thr	Ala	Ala	Leu	Val	Gln	Trp	Pro	Asp	Gln	435	440	445
Arg	Pro	Ile	Pro	Gly	Ile	Arg	Met	Tyr	Gln	Ile	Gln	Tyr	Asn	Ser	Ser	450	455	460
Ala	Asp	Asp	Ile	Leu	Val	Tyr	Arg	Met	Ile	Pro	Ala	Glu	Ser	Arg	Ser	465	470	475
Phe	Leu	Leu	Thr	Asp	Leu	Ala	Ser	Gly	Arg	Thr	Tyr	Asp	Leu	Cys	Val	485	490	495

Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro
500 505 510

Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly
515 520 525

Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly
530 535 540

Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met
545 550 555 560

Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro
565 570 575

Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro
580 585 590

Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala
595 600 605

His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu
610 615 620

Pro Val Gly Pro
625

<210> 7

<211> 802

<212> DNA

<213> Equus caballus

<400> 7

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ttttcccat ggccctcctg ccctctctct tgacggccct ggtggtgtac gagttatggc 180
cctgtggagc tctgggctgt gacctgcctc agaaccacat cctgggttagc aggaagaact 240
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cagcaaact gcaaggaagg ttaagaatga aggatggaga cctgggctca ccttgaaatg 720
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<210> 8

<211> 195

<212> PRT

<213> Homo sapiens

<400> 8

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Ser	Pro	Val	Gly	Ser	Leu	Gly	Cys	Asp	Leu	Pro	Gln	Asn	His	Gly	Leu
			20					25					30		

Leu	Ser	Arg	Asn	Thr	Leu	Val	Leu	Leu	His	Gln	Met	Arg	Arg	Ile	Ser
		35					40					45			

Pro	Phe	Leu	Cys	Leu	Lys	Asp	Arg	Arg	Asp	Phe	Arg	Phe	Pro	Gln	Glu
	50					55					60				

Met	Val	Lys	Gly	Ser	Gln	Leu	Gln	Lys	Ala	His	Val	Met	Ser	Val	Leu
65					70					75					80

His	Glu	Met	Leu	Gln	Gln	Ile	Phe	Ser	Leu	Phe	His	Thr	Glu	Arg	Ser
			85						90					95	

Ser	Ala	Ala	Trp	Asn	Met	Thr	Leu	Leu	Asp	Gln	Leu	His	Thr	Gly	Leu
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His	Gln	Gln	Leu	Gln	His	Leu	Glu	Thr	Cys	Leu	Leu	Gln	Val	Val	Gly
	115						120					125			

Glu	Gly	Glu	Ser	Ala	Gly	Ala	Ile	Ser	Ser	Pro	Ala	Leu	Thr	Leu	Arg
	130					135					140				

Arg	Tyr	Phe	Gln	Gly	Ile	Arg	Val	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser
145					150					155					160

Asp	Cys	Ala	Trp	Glu	Val	Val	Arg	Met	Glu	Ile	Met	Lys	Ser	Leu	Phe
			165						170						175

Leu	Ser	Thr	Asn	Met	Gln	Glu	Arg	Leu	Arg	Ser	Lys	Asp	Arg	Asp	Leu
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Gly	Ser	Ser
	195	

<210> 9

<211> 195

<212> PRT

<213> Equus caballus

<400> 9

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser
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Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser
35 40 45

Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu
50 55 60

Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu
65 70 75 80

Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu
100 105 110

His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly
115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys
130 135 140

Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser
165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu
180 185 190

Gly Ser Pro
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<210> 10

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00143

Domain 71-187

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Ile	Phe	His	Phe	Phe	Cys	Thr	Glu	Ala	Ser	Ser	Ser	Ala	Ala	Trp	Asn
			20					25					30		

Thr	Thr	Leu	Leu	Glu	Glu	Phe	Cys	Thr	Gly	Leu	Asp	Arg	Gln	Leu	Thr
		35					40					45			

Arg	Leu	Glu	Ala	Cys	Val	Leu	Gln	Glu	Val	Glu	Glu	Gly	Glu	Ala	Pro
	50					55					60				

Leu	Thr	Asn	Glu	Asp	Ile	His	Pro	Glu	Asp	Ser	Ile	Leu	Arg	Asn	Tyr
65					70					75				80	

Phe	Gln	Arg	Leu	Ser	Leu	Tyr	Leu	Gln	Glu	Lys	Lys	Tyr	Ser	Pro	Cys
				85					90					95	

Ala	Trp	Glu	Ile	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Leu	Tyr	Tyr	Ser
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Ser	Thr	Ala	Leu	Gln
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<210> 11

<211> 194

<212> PRT

<213> Felis catus

<400> 11

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Asn	Ser	Val	Cys	Ser	Leu	Gly	Cys	Asp	Leu	Pro	Gln	Thr	His	Gly	Leu
			20					25					30		

Leu	Asn	Arg	Arg	Ala	Leu	Thr	Leu	Leu	Gly	Gln	Met	Arg	Arg	Leu	Pro
		35						40				45			

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val
115 120 125

Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser
180 185 190

Glu Lys

<210> 12

<211> 195

<212> PRT

<213> Homo sapiens

<400> 12

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr
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Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu
20 25 30

Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser
35 40 45

Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu

50	55	60
Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu		
65	70	75 80
His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser		
	85 90	95
Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu		
	100 105	110
His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly		
	115 120	125
Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys		
	130 135	140
Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser		
145	150 155	160
Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser		
	165 170	175
Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu		
	180 185	190
Ser Ser Pro		
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<210> 13
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 <212> PRT
 <213> Equus caballus

<400> 13
Met Ala Leu Leu Pro Ser Leu Leu Thr Ala Leu Val Val Tyr Glu Leu
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20 25 30
Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser
35 40 45
Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp
50 55 60

Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu
100 105 110

Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly
115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys
130 135 140

Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser
165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu
180 185 190

Gly Ser Pro
195

<210> 14
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<212> PRT
<213> Homo sapiens

<400> 14
Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
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Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

<210> 15

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus
sequence

<400> 15

Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser
1 5 10 15

Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln
20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys
35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu
50 55 60

Gln
65

<210> 16
<211> 166
<212> PRT
<213> Homo sapiens

<400> 16
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1 5 10 15
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
20 25 30
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
35 40 45
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
50 55 60
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
65 70 75 80
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
85 90 95
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
100 105 110
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
115 120 125
Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
130 135 140
Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
145 150 155 160
Thr Gly Tyr Leu Arg Asn
165

<210> 17
<211> 165
<212> PRT
<213> Homo sapiens

<400> 17

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn
100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145 150 155 160

Leu Arg Ser Lys Glu
165

<210> 18

<211> 189

<212> PRT

<213> Mus musculus

<400> 18

Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr
1 5 10 15

Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu
20 25 30

Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser
 35 40 45

Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu
 50 55 60

Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu
 65 70 75 80

Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser
 85 90 95

Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu
 100 105 110

His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly
 115 120 125

Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg
 130 135 140

Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser
 145 150 155 160

Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser
 165 170 175

Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys
 180 185

<210> 19
 <211> 195
 <212> PRT
 <213> Antilocapra americana

<400> 19
 Met Ala Gln Leu Leu Pro Leu Leu Thr Ala Leu Val Leu Cys Ser Tyr
 1 5 10 15

Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro
 20 25 30

Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser
 35 40 45

Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu
 50 55 60

Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser
85 90 95

Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu
100 105 110

His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly
115 120 125

Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys
130 135 140

Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser
145 150 155 160

Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser
165 170 175

Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu
180 185 190

Ala Ser Ser
195

<210> 20

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus
sequence

<400> 20

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val
35 40

<210> 21
 <211> 184
 <212> PRT
 <213> Equus caballus

<400> 21
 Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys
 1 5 10 15
 His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu
 20 25 30
 Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser
 35 40 45
 Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu
 50 55 60
 Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val
 65 70 75 80
 His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser
 85 90 95
 Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu
 100 105 110
 Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly
 115 120 125
 Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg
 130 135 140
 Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
 145 150 155 160
 Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser
 165 170 175
 Ser Ser Thr Asn Leu Pro Gln Ser
 180

<210> 22
 <211> 92
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus
sequence

<400> 22

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln
85 90

<210> 23

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 23

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tctgaacttg aagacacccc acattccaag atgcccaggg ttctctggga tgctgggggt 120
tcttcgatcc ggaaaatcct accggcatcc tcttagggag ggattattat tattattttt 180
ctttaatctg gaagagaaga gaacaagttg tgcttttccc cccttcttct tgctaaacgc 240
catggatata actgaataag cggctcaggg ctttccccgc gtggacgtcc gaggccacca 300
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gccgggggta gatgctgcct cgcccaggcg ctgagtgacc agaccatgga gacctgctt 480
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gtctgccaga atctgtctga gtcactgggg acctgtgcc cctccaaggg gctgctctt 600
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gcaagcggct ttggattgct tatg 3144

<210> 24
<211> 832
<212> PRT
<213> Homo sapiens

<400> 24
Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser
1 5 10 15
Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg

	20		25		30
Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu					
	35		40		45
Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys					
	50		55		60
Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu					
	65		70		75
Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg					
		85		90	95
Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg					
	100		105		110
Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg					
	115		120		125
Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser					
	130		135		140
Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu					
	145		150		155
Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn					
		165		170	175
Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu					
	180		185		190
Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro					
	195		200		205
Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp					
	210		215		220
His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln					
	225		230		235
Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro					
		245		250	255
Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr					
	260		265		270
Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His					

275		280		285
Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp				
290		295		300
Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp				
305		310		320
His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln				
	325		330	335
His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys				
	340		345	350
Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro				
	355		360	365
Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn				
	370		375	380
Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe				
385		390		400
Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu				
	405		410	415
Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr				
	420		425	430
Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr				
	435		440	445
Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu Pro Pro Lys Ser Pro				
	450		455	460
Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala Leu				
465		470		480
Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln				
	485		490	495
Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile				
	500		505	510
Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr				
	515		520	525
Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr				

530		535		540
Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala				
545		550		555 560
Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr				
	565		570	575
Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val Phe				
	580		585	590
Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro				
	595		600	605
Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly				
	610		615	620
Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln				
625		630		635 640
Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala				
	645		650	655
Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly Ser				
	660		665	670
Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser				
	675		680	685
Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala				
	690		695	700
Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg				
705		710		715 720
Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser				
	725		730	735
Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser Leu				
	740		745	750
Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe Asp				
	755		760	765
Met Gly Asp Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro Gly Gly				
	770		775	780
Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser Leu				

785		790		795		800
Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val Gly						
	805		810		815	
Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr Val						
	820		825		830	

<210> 25
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:IFAbd Domain
 13-110

<400> 25
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
1 5 10 15
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
20 25 30
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
35 40 45
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
50 55 60
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
65 70 75 80
Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
85 90 95

Ile Val

<210> 26
 <211> 183
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00143

Domain 5-187

<400> 26

Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys
1 5 10 15

Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg
20 25 30

Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys
35 40 45

Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly
50 55 60

Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn
65 70 75 80

Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala
85 90 95

Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln
100 105 110

Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu
115 120 125

Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg
130 135 140

Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr
165 170 175

Tyr Ser Ser Thr Ala Leu Gln
180